

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Maertens, Geert
Bosman, Fons
De Martynoff, Guy
Buyse, Marie-Ange
- (ii) TITLE OF INVENTION: Purified hepatitis C virus envelope
proteins for diagnostic and therapeutic use.
- (iii) NUMBER OF SEQUENCES: 122
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: NIXON & VANDERHYE
 - (B) STREET: 1100 North Glebe Road, 8th Floor
 - (C) CITY: Arlington, VA 22201
 - (E) COUNTRY: USA
 - (F) ZIP: 22201
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: Unassigned
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Sadoff, B. J.
 - (B) REGISTRATION NUMBER: 36663
 - (C) REFERENCE/DOCKET NUMBER: 2551-61
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (703) 816-4000
 - (B) TELEFAX: (703) 816-4100

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCATGCAAG CTTAATTAAT T

21

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CCGGGGAGGC CTGCACGTGA TCGAGGGCAG ACACCATCAC CACCATCACT AATAGTTAAT
TAACTGCA

60

68

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 642 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..639

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTA CTG TCC TGT
Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Ala Leu Leu Ser Cys
1 5 10 15

48

CTG ACC ATT CCA GCT TCC GCT TAT GAG GTG CGC AAC GTG TCC GGG ATG
Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Met
20 25 30

96

TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG TAT GAG GCA
Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala

144

35	40	45	
GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG			192
Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu			
50	55	60	
AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG CTC GCA GCT			240
Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala			
65	70	75	80
AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC GTC GAT TTG			288
Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu			
	85	90	95
CTC GTT GGG GCG GCT GCT CTC TGT TCC GCT ATG TAC GTG GGG GAT CTC			336
Leu Val Gly Ala Ala Ala Leu Cys Ser Ala Met Tyr Val Gly Asp Leu			
	100	105	110
TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC TCG CCT CGC			384
Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile Ser Pro Arg			
	115	120	125
CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC			432
Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His			
	130	135	140
ATA ACA GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT			480
Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro			
	145	150	155
ACA ACG GCC CTG GTG GTA TCG CAG CTG CTC CGG ATC CCA CAA GCT GTC			528
Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val			
	165	170	175
GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG GGC CTC GCC			576
Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala			
	180	185	190
TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT GTG ATG CTA			624
Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu			
	195	200	205
CTC TTT GCT CTC TAATAG			642
Leu Phe Ala Leu			
210			

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys
1				5					10					15	
Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Met

(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG	240
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	
TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG	288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC	336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
100 105 110	
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
115 120 125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC	432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His	
130 135 140	
GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TGT TCC GCT ATG TAC GTG	480
Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val	
145 150 155 160	
GGG GAC CTC TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC	528
Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile	
165 170 175	
TCG CCT CGC CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT	576
Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr	
180 185 190	
CCC GGC CAC ATA ACG GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC	624
Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn	
195 200 205	
TGG TCG CCT ACA ACG GCC CTG GTG GTA TCG CAG CTG CTC CGG ATC CCA	672
Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro	
210 215 220	
CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG	720
Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala	
225 230 235 240	
GGT CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT	768

Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile
 245 250 255

GTG ATG CTA CTC TTT GCT CCC TAATAG
 Val Met Leu Leu Phe Ala Pro
 260

795

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu
 1 5 10 15

Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg
 20 25 30

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala
 35 40 45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu
 50 55 60

Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val
 65 70 75 80

Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val
 85 90 95

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys
 100 105 110

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
 115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His
 130 135 140

Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val
 145 150 155 160

Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile
 165 170 175

Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr
 180 185 190

Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn
 195 200 205

Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 210 215 220

Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala

(2) INFORMATION FOR SEQ ID NO: 7:

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..630

(ix) FEATURE:

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(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..627
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(xi) SEQUENCE DESCRIPTION: SEO ID NO: 7:

ATG	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTT	ACG	TGC	GGC	TTC	GCC	GAC	CTC	48
Met	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu	
1				5					10					15		
ATG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCC	CTA	GGG	GGT	GCT	GCC	AGA	96
Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	
			20					25					30			
GCC	CTG	GCG	CAT	GGC	GTC	CGG	GTT	CTG	GAA	GAC	GGC	GTG	AAC	TAT	GCA	144
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	
		35					40					45				
ACA	GGG	AAT	TTG	CCT	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	TTG	GCT	TTA	192
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	
	50					55					60					
CTG	TCC	TGT	CTG	ACC	ATT	CCA	GCT	TCC	GCT	TAT	GAG	GTG	CGC	AAC	GTG	240
Leu	Ser	Cys	Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	
65					70					75					80	
TCC	GGG	ATG	TAC	CAT	GTC	ACG	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATT	GTG	288
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	
				85					90					95		
TAT	GAG	GCA	GCG	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	336
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	
			100					105					110			

GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
115 120 125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACT ACG ACA ATA CGA CGC CAC	432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His	
130 135 140	
GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TGT TCC GCT ATG TAC GTG	480
Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val	
145 150 155 160	
GGG GAT CTC TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC	528
Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile	
165 170 175	
TCG CCT CGC CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT	576
Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr	
180 185 190	
CCC GGC CAC ATA ACA GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC	624
Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn	
195 200 205	
TGG TAATAG	633
Trp	
210	

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
Leu Ser Cys Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
100 105 110	

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
 115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His
 130 135 140

Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val
 145 150 155 160

Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile
 165 170 175

Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr
 180 185 190

Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn
 195 200 205

Trp

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 483 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..480

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCC CTG CTG TCC TGT	48
Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys	
1 5 10 15	
CTG ACC ATA CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG TCC GGG GTG	96
Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val	
20 25 30	
TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATA GTG TAT GAG GCA	144
Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala	
35 40 45	
GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG	192
Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu	
50 55 60	

GGC AAC TCC TCC CGT TGC TGG GTG GCG CTC ACT CCC ACG CTC GCG GCC	240
Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala	
65 70 75 80	
AGG AAC GCC AGC GTC CCC ACA ACG ACA ATA CGA CGC CAC GTC GAT TTG	288
Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu	
85 90 95	
CTC GTT GGG GCT GCT GCT TTC TGT TCC GCT ATG TAC GTG GGG GAT CTC	336
Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu	
100 105 110	
TGC GGA TCT GTT TTC CTT GTT TCC CAG CTG TTC ACC TTC TCA CCT CGC	384
Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg	
115 120 125	
CGG CAT CAA ACA GTA CAG GAC TGC AAC TGC TCA ATC TAT CCC GGC CAT	432
Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His	
130 135 140	
GTA TCA GGT CAC CGC ATG GCT TGG GAT ATG ATG ATG AAC TGG TCC TAATAG	483
Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser	
145 150 155 160	

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys	
1 5 10 15	
Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val	
20 25 30	
Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala	
35 40 45	
Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu	
50 55 60	
Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala	
65 70 75 80	
Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu	
85 90 95	
Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu	
100 105 110	
Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg	
115 120 125	
Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His	

130		135		140
Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser				
145		150		155

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..477

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATG TCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCC CTG CTG TCC TGT	48
Met Ser Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys	
1 5 10 15	
CTG ACC ATA CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG TCC GGG GTG	96
Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val	
20 25 30	
TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATA GTG TAT GAG GCA	144
Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala	
35 40 45	
GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG	192
Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu	
50 55 60	
GGC AAC TCC TCC CGT TGC TGG GTG GCG CTC ACT CCC ACG CTC GCG GCC	240
Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala	
65 70 75 80	
AGG AAC GCC AGC GTC CCC ACA ACG ACA ATA CGA CGC CAC GTC GAT TTG	288
Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu	
85 90 95	
CTC GTT GGG GCT GCT GCT TTC TGT TCC GCT ATG TAC GTG GGG GAT CTC	336
Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu	
100 105 110	
TGC GGA TCT GTT TTC CTT GTT TCC CAG CTG TTC ACC TTC TCA CCT CGC	384
Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg	

115	120	125	
CGG CAT CAA ACA GTA CAG GAC TGC AAC TGC TCA ATC TAT CCC GGC CAT			432
Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His			
130	135	140	
GTA TCA GGT CAC CGC ATG GCT TGG GAT ATG ATG ATG AAC TGG TAATAG			480
Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp			
145	150	155	

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met	Ser	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys
1				5					10					15	
Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val
			20					25					30		
Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala
		35				40						45			
Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu
	50					55					60				
Gly	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala
65				70					75				80		
Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu
			85						90				95		
Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu
		100						105					110		
Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg
		115					120					125			
Arg	His	Gln	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His
130					135						140				
Val	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp		
145					150					155					

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..633

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 1..630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATG	CTG	GGT	AAG	GCC	ATC	GAT	ACC	CTT	ACG	TGC	GGC	TTC	GCC	GAC	CTC	48
Met	Leu	Gly	Lys	Ala	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu	
1				5					10					15		
GTG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCC	CTA	GGG	GGC	GCT	GCC	AGG	96
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	
			20					25					30			
GCC	CTG	GCG	CAT	GGC	GTC	CGG	GTT	CTG	GAA	GAC	GGC	GTG	AAC	TAT	GCA	144
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	
		35				40						45				
ACA	GGG	AAT	TTG	CCT	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	TTG	GCT	TTA	192
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	
	50				55					60						
CTG	TCC	TGT	CTA	ACC	ATT	CCA	GCT	TCC	GCT	TAC	GAG	GTG	CGC	AAC	GTG	240
Leu	Ser	Cys	Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	
65				70				75						80		
TCC	GGG	ATG	TAC	CAT	GTC	ACG	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATT	GTG	288
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	
				85				90						95		
TAT	GAG	GCA	GCG	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	336
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	
			100					105					110			
GTT	CGG	GAG	AAC	AAC	TCT	TCC	CGC	TGC	TGG	GTA	GCG	CTC	ACC	CCC	ACG	384
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	
		115					120					125				
CTC	GCG	GCT	AGG	AAC	GCC	AGC	ATC	CCC	ACT	ACA	ACA	ATA	CGA	CGC	CAC	432
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Ile	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	
	130				135							140				
GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	GCT	TTC	TGT	TCC	GCT	ATG	TAC	GTG	480
Val	Asp	Leu	Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	
145				150						155				160		
GGG	GAT	CTC	TGC	GGA	TCT	GTC	TTC	CTC	GTC	TCC	CAG	CTG	TTC	ACC	ATC	528
Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile	
			165					170						175		
TCG	CCT	CGC	CGG	CAT	GAG	ACG	GTG	CAG	GAC	TGC	AAT	TGC	TCA	ATC	TAT	576
Ser	Pro	Arg	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	

180	185	190	
CCC GGC CAC ATA ACG GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC			624
Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn			
195	200	205	
TGG TAC TAATAG			640
Trp Tyr			
210			

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met	Leu	Gly	Lys	Ala	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu	
1				5				10						15		
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	
			20					25					30			
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	
		35					40					45				
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	
	50					55					60					
Leu	Ser	Cys	Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	
65					70					75				80		
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	
				85					90					95		
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	
			100					105					110			
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	
			115				120					125				
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Ile	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	
			130				135					140				
Val	Asp	Leu	Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	
145					150				155					160		
Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile	
			165					170					175			
Ser	Pro	Arg	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	
			180					185					190			
Pro	Gly	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	
		195					200					205				

Trp Tyr
210

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ATGCCCGGTT GCTCTTCTC TATCTT

26

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ATGTTGGGTA AGGTCATCGA TACCCT

26

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CTATTAGGAC CAGTTCATCA TCATATCCCA

30

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CTATTACCAG TTCATCATCA TATCCCA

27

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ATACGACGCC ACGTCGATTC CCAGCTGTTC ACCATC

36

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GATGGTGAAC AGCTGGGAAT CGACGTGGCG TCGTAT

36

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 723 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..720

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG	240
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	
TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG	288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC	336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
100 105 110	
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
115 120 125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC	432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His	
130 135 140	
GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG	480
Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val	

145		150		155		160	
CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT							528
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg							
	165			170		175	
ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG							576
Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val							
	180			185		190	
GTA TCG CAG CTG CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG							624
Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala							
	195			200		205	
GGG GCC CAT TGG GGA GTC CTG GCG GGT CTC GCC TAC TAT TCC ATG GTG							672
Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val							
	210			215		220	
GGG AAC TGG GCT AAG GTT TTG ATT GTG ATG CTA CTC TTT GCT CCC TAATAG							723
Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu Leu Phe Ala Pro							
	225			230		235	240

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu
1				5				10						15	
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg
			20					25					30		
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala
			35				40					45			
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu
			50			55					60				
Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val
			65		70					75				80	
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val
				85					90					95	
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys
			100					105					110		
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr
			115				120					125			
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His
			130				135					140			
Val	Asp	Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	Arg	His	Glu	Thr	Val

145		150		155		160
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg						
	165			170		175
Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val						
	180			185		190
Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala						
	195			200		205
Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val						
	210			215		220
Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu Leu Phe Ala Pro						
225		230		235		

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..558

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG	240
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	

65	70	75	80	
TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG				288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	85	90	95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC				336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	100	105	110	
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG				384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	115	120	125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC				432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His	130	135	140	
GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG				480
Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val	145	150	155	160
CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT				528
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg	165	170	175	
ATG GCT TGG GAT ATG ATG ATG AAC TGG TAATAG				561
Met Ala Trp Asp Met Met Met Asn Trp	180	185		

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Met	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu
1				5				10						15	
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg
			20					25					30		
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala
		35					40					45			
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu
		50				55					60				
Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val
	65				70				75					80	
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val
				85				90						95	
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys
			100					105					110		

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
 115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His
 130 135 140

Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val
 145 150 155 160

Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg
 165 170 175

Met Ala Trp Asp Met Met Met Asn Trp
 180 185

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 606 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..603

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG	240
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	

TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG	288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC	336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
100 105 110	
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
115 120 125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC	432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His	
130 135 140	
GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG	480
Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val	
145 150 155 160	
CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT	528
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg	
165 170 175	
ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG	576
Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val	
180 185 190	
GTA TCG CAG CTG CTC CGG ATC CTC TAATAG	606
Val Ser Gln Leu Leu Arg Ile Leu	
195 200	

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys
 100 105 110
 Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
 115 120 125
 Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His
 130 135 140
 Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val
 145 150 155 160
 Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg
 165 170 175
 Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val
 180 185 190
 Val Ser Gln Leu Leu Arg Ile Leu
 195 200

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 636 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..633

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192

Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu		
	50					55					60						
CTG	TCC	TGT	CTG	ACC	GTT	CCA	GCT	TCC	GCT	TAT	GAA	GTG	CGC	AAC	GTG		240
Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val		
	65				70					75					80		
TCC	GGG	ATG	TAC	CAT	GTC	ACG	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATT	GTG		288
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val		
				85					90					95			
TAT	GAG	GCA	GCG	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC		336
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys		
			100					105					110				
GTT	CGG	GAG	AAC	AAC	TCT	TCC	CGC	TGC	TGG	GTA	GCG	CTC	ACC	CCC	ACG		384
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr		
		115					120					125					
CTC	GCA	GCT	AGG	AAC	GCC	AGC	GTC	CCC	ACC	ACG	ACA	ATA	CGA	CGC	CAC		432
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His		
	130						135					140					
GTC	GAT	TCC	CAG	CTG	TTC	ACC	ATC	TCG	CCT	CGC	CGG	CAT	GAG	ACG	GTG		480
Val	Asp	Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	Arg	His	Glu	Thr	Val		
	145				150					155					160		
CAG	GAC	TGC	AAT	TGC	TCA	ATC	TAT	CCC	GGC	CAC	ATA	ACG	GGT	CAC	CGT		528
Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	Ile	Thr	Gly	His	Arg		
				165					170					175			
ATG	GCT	TGG	GAT	ATG	ATG	ATG	AAC	TGG	TCG	CCT	ACA	ACG	GCC	CTG	GTG		576
Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	Ser	Pro	Thr	Thr	Ala	Leu	Val		
			180					185					190				
GTA	TCG	CAG	CTG	CTC	CGG	ATC	GTG	ATC	GAG	GGC	AGA	CAC	CAT	CAC	CAC		624
Val	Ser	Gln	Leu	Leu	Arg	Ile	Val	Ile	Glu	Gly	Arg	His	His	His	His		
		195				200					205						
CAT	CAC	TAATAG															636
His	His																
	210																

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 210 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu		
1				5				10						15			
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg		
		20					25					30					
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala		

35					40					45					
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu
50						55					60				
Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val
65					70					75				80	
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val
				85					90					95	
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys
			100					105					110		
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr
			115				120					125			
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His
			130				135					140			
Val	Asp	Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	Arg	His	Glu	Thr	Val
145					150					155				160	
Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	Ile	Thr	Gly	His	Arg
			165						170				175		
Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	Ser	Pro	Thr	Thr	Ala	Leu	Val
			180					185					190		
Val	Ser	Gln	Leu	Leu	Arg	Ile	Val	Ile	Glu	Gly	Arg	His	His	His	His
			195				200					205			
His	His														
			210												

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 630 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..627

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

ATG GGT AAG GTC ATC GAT ACC CTT ACG TGC GGA TTC GCC GAT CTC ATG

Met	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	
1				5					10					15		
GGG	TAC	ATC	CCG	CTC	GTC	GGC	GCT	CCC	GTA	GGA	GGC	GTC	GCA	AGA	GCC	96
Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	
			20					25					30			
CTT	GCG	CAT	GGC	GTG	AGG	GCC	CTT	GAA	GAC	GGG	ATA	AAT	TTC	GCA	ACA	144
Leu	Ala	His	Gly	Val	Arg	Ala	Leu	Glu	Asp	Gly	Ile	Asn	Phe	Ala	Thr	
		35					40					45				
GGG	AAT	TTG	CCC	GGT	TGC	TCC	TTT	TCT	ATT	TTC	CTT	CTC	GCT	CTG	TTC	192
Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Phe	
	50					55					60					
TCT	TGC	TTA	ATT	CAT	CCA	GCA	GCT	AGT	CTA	GAG	TGG	CGG	AAT	ACG	TCT	240
Ser	Cys	Leu	Ile	His	Pro	Ala	Ala	Ser	Leu	Glu	Trp	Arg	Asn	Thr	Ser	
	65				70					75					80	
GGC	CTC	TAT	GTC	CTT	ACC	AAC	GAC	TGT	TCC	AAT	AGC	AGT	ATT	GTG	TAC	288
Gly	Leu	Tyr	Val	Leu	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	
			85						90					95		
GAG	GCC	GAT	GAC	GTT	ATT	CTG	CAC	ACA	CCC	GGC	TGC	ATA	CCT	TGT	GTC	336
Glu	Ala	Asp	Gly	Val	Ile	Leu	His	Thr	Pro	Gly	Cys	Ile	Pro	Cys	Val	
			100					105					110			
CAG	GAC	GGC	AAT	ACA	TCC	ACG	TGC	TGG	ACC	CCA	GTG	ACA	CCT	ACA	GTG	384
Gln	Asp	Gly	Asn	Thr	Ser	Thr	Cys	Trp	Thr	Pro	Val	Thr	Pro	Thr	Val	
		115					120					125				
GCA	GTC	AAG	TAC	GTC	GGA	GCA	ACC	ACC	GCT	TCG	ATA	CGC	AGT	CAT	GTG	432
Ala	Val	Lys	Tyr	Val	Gly	Ala	Thr	Thr	Ala	Ser	Ile	Arg	Ser	His	Val	
		130				135						140				
GAC	CTA	TTA	GTG	GGC	GCG	GCC	ACG	ATG	TGC	TCT	GCG	CTC	TAC	GTG	GGT	480
Asp	Leu	Leu	Val	Gly	Ala	Ala	Thr	Met	Cys	Ser	Ala	Leu	Tyr	Val	Gly	
	145				150					155					160	
GAC	ATG	TGT	GGG	GCT	GTC	TTC	CTC	GTG	GGA	CAA	GCC	TTC	ACG	TTC	AGA	528
Asp	Met	Cys	Gly	Ala	Val	Phe	Leu	Val	Gly	Gln	Ala	Phe	Thr	Phe	Arg	
			165					170						175		
CCT	CGT	CGC	CAT	CAA	ACG	GTC	CAG	ACC	TGT	AAC	TGC	TCG	CTG	TAC	CCA	576
Pro	Arg	Arg	His	Gln	Thr	Val	Gln	Thr	Cys	Asn	Cys	Ser	Leu	Tyr	Pro	
			180					185					190			
GGC	CAT	CTT	TCA	GGA	CAT	CGA	ATG	GCT	TGG	GAT	ATG	ATG	ATG	AAC	TGG	624
Gly	His	Leu	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
		195					200						205			
TAATAG																634

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 208 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```

Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met
 1           5           10           15
Gly Tyr Ile Pro Leu Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala
          20           25           30
Leu Ala His Gly Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr
          35           40           45
Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe
          50           55           60
Ser Cys Leu Ile His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser
          65           70           75           80
Gly Leu Tyr Val Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr
          85           90           95
Glu Ala Asp Asp Val Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val
          100          105          110
Gln Asp Gly Asn Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val
          115          120          125
Ala Val Lys Tyr Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val
          130          135          140
Asp Leu Leu Val Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly
          145          150          155          160
Asp Met Cys Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg
          165          170          175
Pro Arg Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro
          180          185          190
Gly His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
          195          200          205

```

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..627

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATG GGT AAG GTC ATC GAT ACC CTA ACG TGC GGA TTC GCC GAT CTC ATG	48
Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met	
1 5 10 15	
GGG TAT ATC CCG CTC GTA GGC GGC CCC ATT GGG GGC GTC GCA AGG GCT	96
Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile Gly Gly Val Ala Arg Ala	
20 25 30	
CTC GCA CAC GGT GTG AGG GTC CTT GAG GAC GGG GTA AAC TAT GCA ACA	144
Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr	
35 40 45	
GGG AAT TTA CCC GGT TGC TCT TTC TCT ATC TTT ATT CTT GCT CTT CTC	192
Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu	
50 55 60	
TGC TGT CTG ACC GTT CCG GCC TCT GCA GTT CCC TAC CGA AAT GCC TCT	240
Ser Cys Leu Thr Val Pro Ala Ser Ala Val Pro Tyr Arg Asn Ala Ser	
65 70 75 80	
GGG ATT TAT CAT GTT ACC AAT GAT TGC CCA AAC TCT TCC ATA GTC TAT	288
Gly Ile Tyr His Val Thr Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr	
85 90 95	
GAG GCA GAT AAC CTG ATC CTA CAC GCA CCT GGT TGC GTG CCT TGT GTC	336
Glu Ala Asp Asn Leu Ile Leu His Ala Pro Gly Cys Val Pro Cys Val	
100 105 110	
ATG ACA GGT AAT GTG AGT AGA TGC TGG GTC CAA ATT ACC CCT ACA CTG	384
Met Thr Gly Asn Val Ser Arg Cys Trp Val Gln Ile Thr Pro Thr Leu	
115 120 125	
TCA GCC CCG AGC CTC GGA GCA GTC ACG GCT CCT CTT CGG AGA GCC GTT	432
Ser Ala Pro Ser Leu Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val	
130 135 140	
GAC TAC CTA GCG GGA GGG GCT GCC CTC TGC TCC GCG TTA TAC GTA GGA	480
Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly	
145 150 155 160	
GAC GCG TGT GGG GCA CTA TTC TTG GTA GGC CAA ATG TTC ACC TAT AGG	528
Asp Ala Cys Gly Ala Leu Phe Leu Val Gly Gln Met Phe Thr Tyr Arg	
165 170 175	
CCT CGC CAG CAC GCT ACG GTG CAG AAC TGC AAC TGT TCC ATT TAC AGT	576
Pro Arg Gln His Ala Thr Val Gln Asn Cys Asn Cys Ser Ile Tyr Ser	
180 185 190	
GGC CAT GTT ACC GGC CAC CGG ATG GCA TGG GAT ATG ATG ATG AAC TGG	624
Gly His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp	
195 200 205	

TAATAG

630

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```

Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met
 1           5           10           15
Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile Gly Gly Val Ala Arg Ala
 20           25           30
Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr
 35           40           45
Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu
 50           55           60
Ser Cys Leu Thr Val Pro Ala Ser Ala Val Pro Tyr Arg Asn Ala Ser
 65           70           75           80
Gly Ile Tyr His Val Thr Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr
 85           90           95
Glu Ala Asp Asn Leu Ile Leu His Ala Pro Gly Cys Val Pro Cys Val
100           105           110
Met Thr Gly Asn Val Ser Arg Cys Trp Val Gln Ile Thr Pro Thr Leu
115           120           125
Ser Ala Pro Ser Leu Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val
130           135           140
Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly
145           150           155           160
Asp Ala Cys Gly Ala Leu Phe Leu Val Gly Gln Met Phe Thr Tyr Arg
165           170           175
Pro Arg Gln His Ala Thr Val Gln Asn Cys Asn Cys Ser Ile Tyr Ser
180           185           190
Gly His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
195           200           205

```

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:
 TGGGATATGA TGATGAACTG GTC

23

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:
 CTATTATGGT GGTAAAGCCAC AGAGCAGGAG

30

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1476 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1473

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..1470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:
 TGG GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG GTA TCG

48

Trp	Asp	Met	Met	Met	Asn	Trp	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	
1				5					10					15		
CAG	CTG	CTC	CGG	ATC	CCA	CAA	GCT	GTC	GTG	GAC	ATG	GTG	GCG	GGG	GCC	96
Gln	Leu	Leu	Arg	Ile	Pro	Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	
			20					25					30			
CAT	TGG	GGA	GTC	CTG	GCG	GGC	CTC	GCC	TAC	TAT	TCC	ATG	GTG	GGG	AAC	144
His	Trp	Gly	Val	Leu	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	
		35					40					45				
TGG	GCT	AAG	GTT	TTG	GTT	GTG	ATG	CTA	CTC	TTT	GCC	GGC	GTC	GAC	GGG	192
Trp	Ala	Lys	Val	Leu	Val	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly	
	50					55					60					
CAT	ACC	CGC	GTG	TCA	GGA	GGG	GCA	GCA	GCC	TCC	GAT	ACC	AGG	GGC	CTT	240
His	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Ala	Ser	Asp	Thr	Arg	Gly	Leu	
	65				70					75					80	
GTG	TCC	CTC	TTT	AGC	CCC	GGG	TCG	GCT	CAG	AAA	ATC	CAG	CTC	GTA	AAC	288
Val	Ser	Leu	Phe	Ser	Pro	Gly	Ser	Ala	Gln	Lys	Ile	Gln	Leu	Val	Asn	
				85					90					95		
ACC	AAC	GGC	AGT	TGG	CAC	ATC	AAC	AGG	ACT	GCC	CTG	AAC	TGC	AAC	GAC	336
Thr	Asn	Gly	Ser	Trp	His	Ile	Asn	Arg	Thr	Ala	Leu	Asn	Cys	Asn	Asp	
			100					105					110			
TCC	CTC	CAA	ACA	GGG	TTC	TTT	GCC	GCA	CTA	TTC	TAC	AAA	CAC	AAA	TTC	384
Ser	Leu	Gln	Thr	Gly	Phe	Phe	Ala	Ala	Leu	Phe	Tyr	Lys	His	Lys	Phe	
			115				120					125				
AAC	TCG	TCT	GGA	TGC	CCA	GAG	CGC	TTG	GCC	AGC	TGT	CGC	TCC	ATC	GAC	432
Asn	Ser	Ser	Gly	Cys	Pro	Glu	Arg	Leu	Ala	Ser	Cys	Arg	Ser	Ile	Asp	
	130					135					140					
AAG	TTC	GCT	CAG	GGG	TGG	GGT	CCC	CTC	ACT	TAC	ACT	GAG	CCT	AAC	AGC	480
Lys	Phe	Ala	Gln	Gly	Trp	Gly	Pro	Leu	Thr	Tyr	Thr	Glu	Pro	Asn	Ser	
	145				150					155					160	
TCG	GAC	CAG	AGG	CCC	TAC	TGC	TGG	CAC	TAC	GCG	CCT	CGA	CCG	TGT	GGT	528
Ser	Asp	Gln	Arg	Pro	Tyr	Cys	Trp	His	Tyr	Ala	Pro	Arg	Pro	Cys	Gly	
				165					170					175		
ATT	GTA	CCC	GCG	TCT	CAG	GTG	TGC	GGT	CCA	GTG	TAT	TGC	TTC	ACC	CCG	576
Ile	Val	Pro	Ala	Ser	Gln	Val	Cys	Gly	Pro	Val	Tyr	Cys	Phe	Thr	Pro	
			180					185					190			
AGC	CCT	GTT	GTG	GTG	GGG	ACG	ACC	GAT	CGG	TTT	GGT	GTC	CCC	ACG	TAT	624
Ser	Pro	Val	Val	Val	Gly	Thr	Thr	Asp	Arg	Phe	Gly	Val	Pro	Thr	Tyr	
			195					200				205				
AAC	TGG	GGG	GCG	AAC	GAC	TCG	GAT	GTG	CTG	ATT	CTC	AAC	AAC	ACG	CGG	672
Asn	Trp	Gly	Ala	Asn	Asp	Ser	Asp	Val	Leu	Ile		Asn	Asn	Thr	Arg	
	210					215					220					
CCG	CCG	CGA	GGC	AAC	TGG	TTC	GGC	TGT	ACA	TGG	ATG	AAT	GGC	ACT	GGG	720
Pro	Pro	Arg	Gly	Asn	Trp	Phe	Gly	Cys	Thr	Trp	Met	Asn	Gly	Thr	Gly	
	225				230					235					240	
TTC	ACC	AAG	ACG	TGT	GGG	GGC	CCC	CCG	TGC	AAC	ATC	GGG	GGG	GCC	GGC	768
Phe	Thr	Lys	Thr	Cys	Gly	Gly	Pro	Pro	Cys	Asn	Ile	Gly	Gly	Ala	Gly	
				245					250					255		

AAC AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG	816
Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu	
260 265 270	
GCC ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT	864
Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys	
275 280 285	
ATG GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC	912
Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn	
290 295 300	
TTC ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG	960
Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg	
305 310 315 320	
TTC GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG	1008
Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu	
325 330 335	
GAC AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG CTG TCT ACA ACA GAG	1056
Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu	
340 345 350	
TGG CAG ATA CTG CCC TGT TCC TTC ACC ACC CTG CCG GCC CTA TCC ACC	1104
Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr	
355 360 365	
GGC CTG ATC CAC CTC CAT CAG AAC ATC GTG GAC GTG CAA TAC CTG TAC	1152
Gly Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr	
370 375 380	
GGT GTA GGG TCG GCG GTT GTC TCC CTT GTC ATC AAA TGG GAG TAT GTC	1200
Gly Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val	
385 390 395 400	
CTG TTG CTC TTC CTT CTC CTG GCA GAC GCG CGC ATC TGC GCC TGC TTA	1248
Leu Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu	
405 410 415	
TGG ATG ATG CTG CTG ATA GCT CAA GCT GAG GCC GCC TTA GAG AAC CTG	1296
Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu	
420 425 430	
GTG GTC CTC AAT GCG GCG GCC GTG GCC GGG GCG CAT GGC ACT CTT TCC	1344
Val Val Leu Asn Ala Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser	
435 440 445	
TTC CTT GTG TTC TTC TGT GCT GCC TGG TAC ATC AAG GGC AGG CTG GTC	1392
Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val	
450 455 460	
CCT GGT GCG GCA TAC GCC TTC TAT GCC GTG TGG CCG CTG CTC CTG CTT	1440
Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu	
465 470 475 480	
CTG CTG GCC TTA CCA CCA CGA GCT TAT GCC TAGTAA	1476
Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala	
485 490	

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```

Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val Val Ser
 1             5             10      15
Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala
 20             25             30
His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn
 35             40             45
Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly
 50             55             60
His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu
 65             70             75             80
Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn
 85             90             95
Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp
100            105            110
Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe
115            120            125
Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp
130            135            140
Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser
145            150            155            160
Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly
165            170            175
Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro
180            185            190
Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr
195            200            205
Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg
210            215            220
Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly
225            230            235            240
Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly
245            250            255
Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu
260            265            270
Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys

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275	280	285
Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn 290 295 300		
Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg 305 310 315 320		
Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu 325 330 335		
Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu 340 345 350		
Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr 355 360 365		
Gly Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr 370 375 380		
Gly Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val 385 390 395 400		
Leu Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu 405 410 415		
Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu 420 425 430		
Val Val Leu Asn Ala Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser 435 440 445		
Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val 450 455 460		
Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu 465 470 475 480		
Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala 485 490		

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1021 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..1018

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide

(B) LOCATION: 2..1015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

G ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA	46
Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly	
1 5 10 15	
GTC CTG GCG GGC CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG	94
Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys	
20 25 30	
GTT TTG GTT GTG ATG CTA CTC TTT GCC GGC GTC GAC GGG CAT ACC CGC	142
Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg	
35 40 45	
GTG TCA GGA GGG GCA GCA GCC TCC GAT ACC AGG GGC CTT GTG TCC CTC	190
Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu	
50 55 60	
TTT AGC CCC GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC ACC AAC GGC	238
Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly	
65 70 75	
AGT TGG CAC ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC TCC CTC CAA	286
Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln	
80 85 90 95	
ACA GGG TTC TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC AAC TCG TCT	334
Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser	
100 105 110	
GGA TGC CCA GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC AAG TTC GCT	382
Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala	
115 120 125	
CAG GGG TGG GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC TCG GAC CAG	430
Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln	
130 135 140	
AGG CCC TAC TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT ATT GTA CCC	478
Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro	
145 150 155	
GCG TCT CAG GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG AGC CCT GTT	526
Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val	
160 165 170 175	
GTG GTG GGG ACG ACC GAT CGG TTT GGT GTC CCC ACG TAT AAC TGG GGG	574
Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly	
180 185 190	
GCG AAC GAC TCG GAT GTG CTG ATT CTC AAC AAC ACG CGG CCG CCG CGA	622
Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg	
195 200 205	
GGC AAC TGG TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC ACC AAG	670
Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys	
210 215 220	
ACG TGT GGG GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC AAC ACC	718
Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr	

225	230	235	
TTG ACC TGC CCC ACT GAC	TGT TTT CGG AAG CAC	CCC GAG GCC ACC TAC	766
Leu Thr Cys Pro Thr Asp	Cys Phe Arg Lys His	Pro Glu Ala Thr Tyr	
240	245	250	255
GCC AGA TGC GGT TCT GGG	CCC TGG CTG ACA CCT	AGG TGT ATG GTT CAT	814
Ala Arg Cys Gly Ser Gly	Pro Trp Leu Thr Pro	Arg Cys Met Val His	
260	265	270	
TAC CCA TAT AGG CTC TGG	CAC TAC CCC TGC ACT	GTC AAC TTC ACC ATC	862
Tyr Pro Tyr Arg Leu Trp	His Tyr Pro Cys Thr	Val Asn Phe Thr Ile	
275	280	285	
TTC AAG GTT AGG ATG TAC	GTG GGG GGC GTG GAG	CAC AGG TTC GAA GCC	910
Phe Lys Val Arg Met Tyr	Val Gly Gly Val Glu	His Arg Phe Glu Ala	
290	295	300	
GCA TGC AAT TGG ACT CGA	GGA GAG CGT TGT GAC	TTG GAG GAC AGG GAT	958
Ala Cys Asn Trp Thr Arg	Gly Glu Arg Cys Asp	Leu Glu Asp Arg Asp	
305	310	315	
AGA TCA GAG CTT AGC CCG	CTG CTG CTG TCT ACA	ACA GAG TGG CAG AGT	1006
Arg Ser Glu Leu Ser Pro	Leu Leu Leu Ser Thr	Thr Glu Trp Gln Ser	
320	325	330	335
GGC AGA GCT TAATTA			1021
Gly Arg Ala			

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 338 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Ile	Pro	Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val
1				5					10					15	
Leu	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val
			20					25					30		
Leu	Val	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly	His	Thr	Arg	Val
		35				40					45				
Ser	Gly	Gly	Ala	Ala	Ala	Ser	Asp	Thr	Arg	Gly	Leu	Val	Ser	Leu	Phe
	50					55					60				
Ser	Pro	Gly	Ser	Ala	Gln	Lys	Ile	Gln	Leu	Val	Asn	Thr	Asn	Gly	Ser
65				70					75					80	
Trp	His	Ile	Asn	Arg	Thr	Ala	Leu	Asn	Cys	Asn	Asp	Ser	Leu	Gln	Thr
			85					90						95	
Gly	Phe	Phe	Ala	Ala	Leu	Phe	Tyr	Lys	His	Lys	Phe	Asn	Ser	Ser	Gly
			100					105					110		

Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln
 115 120 125
 Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg
 130 135 140
 Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala
 145 150 155 160
 Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val
 165 170 175
 Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala
 180 185 190
 Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly
 195 200 205
 Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr
 210 215 220
 Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu
 225 230 235 240
 Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala
 245 250 255
 Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr
 260 265 270
 Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe
 275 280 285
 Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala
 290 295 300
 Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg
 305 310 315 320
 Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp Gln Ser Gly
 325 330 335
 Arg Ala

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1034 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 2..1032

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 2..1029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

G ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA	46
Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly	
1 5 10 15	
GTC CTG GCG GGC CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG	94
Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys	
20 25 30	
GTT TTG GTT GTG ATG CTA CTC TTT GCC GGC GTC GAC GGG CAT ACC CGC	142
Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg	
35 40 45	
GTG TCA GGA GGG GCA GCA GCC TCC GAT ACC AGG GGC CTT GTG TCC CTC	190
Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu	
50 55 60	
TTT AGC CCC GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC ACC AAC GGC	238
Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly	
65 70 75	
AGT TGG CAC ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC TCC CTC CAA	286
Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln	
80 85 90 95	
ACA GGG TTC TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC AAC TCG TCT	334
Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser	
100 105 110	
GGA TGC CCA GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC AAG TTC GCT	382
Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala	
115 120 125	
CAG GGG TGG GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC TCG GAC CAG	430
Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln	
130 135 140	
AGG CCC TAC TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT ATT GTA CCC	478
Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro	
145 150 155	
GCG TCT CAG GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG AGC CCT GTT	526
Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val	
160 165 170 175	
GTG GTG GGG ACG ACC GAT CGG TTT GGT GTC CCC ACG TAT AAC TGG GGG	574
Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly	
180 185 190	
GCG AAC GAC TCG GAT GTG CTG ATT CTC AAC AAC ACG CCG CCG CCG CGA	622
Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg	
195 200 205	

GGC AAC TGG TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC ACC AAG Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys 210 215 220	670
ACG TGT GGG GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC AAC ACC Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr 225 230 235	718
TTG ACC TGC CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG GCC ACC TAC Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr 240 245 250 255	766
GCC AGA TGC GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT ATG GTT CAT Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His 260 265 270	814
TAC CCA TAT AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC TTC ACC ATC Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile 275 280 285	862
TTC AAG GTT AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG TTC GAA GCC Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala 290 295 300	910
GCA TGC AAT TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC AGG GAT Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp 305 310 315	958
AGA TCA GAG CTT AGC CCG CTG CTG CTG TCT ACA ACA GGT GAT CGA GGG Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Gly Asp Arg Gly 320 325 330 335	1006
CAG ACA CCA TCA CCA CCA TCA CTA AT AG Gln Thr Pro Ser Pro Pro Ser Leu 340	1034

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 343 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val 1 5 10 15
Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val 20 25 30
Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val 35 40 45
Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe 50 55 60
Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser 65 70 75 80

Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr
 85 90 95
 Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly
 100 105 110
 Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln
 115 120 125
 Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg
 130 135 140
 Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala
 145 150 155 160
 Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val
 165 170 175
 Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala
 180 185 190
 Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly
 195 200 205
 Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr
 210 215 220
 Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu
 225 230 235 240
 Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala
 245 250 255
 Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr
 260 265 270
 Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe
 275 280 285
 Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala
 290 295 300
 Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg
 305 310 315 320
 Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Gly Asp Arg Gly Gln
 325 330 335
 Thr Pro Ser Pro Pro Ser Leu
 340

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 945 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..942

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 1..939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

ATG GTG GGG AAC TGG GCT AAG GTT TTG GTT GTG ATG CTA CTC TTT GCC	48
Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala	
1 5 10 15	
GGC GTC GAC GGG CAT ACC CGC GTG TCA GGA GGG GCA GCA GCC TCC GAT	96
Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp	
20 25 30	
ACC AGG GGC CTT GTG TCC CTC TTT AGC CCC GGG TCG GCT CAG AAA ATC	144
Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile	
35 40 45	
CAG CTC GTA AAC ACC AAC GGC AGT TGG CAC ATC AAC AGG ACT GCC CTG	192
Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu	
50 55 60	
AAC TGC AAC GAC TCC CTC CAA ACA GGG TTC TTT GCC GCA CTA TTC TAC	240
Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr	
65 70 75 80	
AAA CAC AAA TTC AAC TCG TCT GGA TGC CCA GAG CGC TTG GCC AGC TGT	288
Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys	
85 90 95	
CGC TCC ATC GAC AAG TTC GCT CAG GGG TGG GGT CCC CTC ACT TAC ACT	336
Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr	
100 105 110	
GAG CCT AAC AGC TCG GAC CAG AGG CCC TAC TGC TGG CAC TAC GCG CCT	384
Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro	
115 120 125	
CGA CCG TGT GGT ATT GTA CCC GCG TCT CAG GTG TGC GGT CCA GTG TAT	432
Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr	
130 135 140	
TGC TTC ACC CCG AGC CCT GTT GTG GTG GGG ACG ACC GAT CGG TTT GGT	480
Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly	
145 150 155 160	
GTC CCC ACG TAT AAC TGG GGG GCG AAC GAC TCG GAT GTG CTG ATT CTC	528
Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu	
165 170 175	
AAC AAC ACG CGG CCG CCG CGA GGC AAC TGG TTC GGC TGT ACA TGG ATG	576
Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met	
180 185 190	

AAT GGC ACT GGG TTC ACC AAG ACG TGT GGG GGC CCC CCG TGC AAC ATC Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile 195 200 205	624
GGG GGG GCC GGC AAC AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT CGG Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg 210 215 220	672
AAG CAC CCC GAG GCC ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG CTG Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu 225 230 235 240	720
ACA CCT AGG TGT ATG GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC CCC Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro 245 250 255	768
TGC ACT GTC AAC TTC ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG GGC Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly 260 265 270	816
GTG GAG CAC AGG TTC GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG CGT Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg 275 280 285	864
TGT GAC TTG GAG GAC AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG CTG Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu 290 295 300	912
TCT ACA ACA GAG TGG CAG AGC TTA ATT AAT TAG Ser Thr Thr Glu Trp Gln Ser Leu Ile Asn 305 310	945

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala 1 5 10 15
Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp 20 25 30
Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile 35 40 45
Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu 50 55 60
Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr 65 70 75 80
Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys 85 90 95

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Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr
      100                      105                      110

Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro
      115                      120                      125

Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr
      130                      135                      140

Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly
      145                      150                      155                      160

Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu
      165                      170                      175

Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met
      180                      185                      190

Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile
      195                      200                      205

Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg
      210                      215                      220

Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu
      225                      230                      235                      240

Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro
      245                      250                      255

Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly
      260                      265                      270

Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg
      275                      280                      285

Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu
      290                      295                      300

Ser Thr Thr Glu Trp Gln Ser Leu Ile Asn
      305                      310

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(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 961 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..958

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide

(B) LOCATION: 1..955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

ATG GTG GGG AAC TGG GCT AAG GTT TTG GTT GTG ATG CTA CTC TTT GCC	48
Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala	
1 5 10 15	
GGC GTC GAC GGG CAT ACC CGC GTG TCA GGA GGG GCA GCA GCC TCC GAT	96
Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp	
20 25 30	
ACC AGG GGC CTT GTG TCC CTC TTT AGC CCC GGG TCG GCT CAG AAA ATC	144
Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile	
35 40 45	
CAG CTC GTA AAC ACC AAC GGC AGT TGG CAC ATC AAC AGG ACT GCC CTG	192
Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu	
50 55 60	
AAC TGC AAC GAC TCC CTC CAA ACA GGG TTC TTT GCC GCA CTA TTC TAC	240
Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr	
65 70 75 80	
AAA CAC AAA TTC AAC TCG TCT GGA TGC CCA GAG CGC TTG GCC AGC TGT	288
Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys	
85 90 95	
CGC TCC ATC GAC AAG TTC GCT CAG GGG TGG GGT CCC CTC ACT TAC ACT	336
Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr	
100 105 110	
GAG CCT AAC AGC TCG GAC CAG AGG CCC TAC TGC TGG CAC TAC GCG CCT	384
Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro	
115 120 125	
CGA CCG TGT GGT ATT GTA CCC GCG TCT CAG GTG TGC GGT CCA GTG TAT	432
Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr	
130 135 140	
TGC TTC ACC CCG AGC CCT GTT GTG GTG GGG ACG ACC GAT CGG TTT GGT	480
Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly	
145 150 155 160	
GTC CCC ACG TAT AAC TGG GGG GCG AAC GAC TCG GAT GTG CTG ATT CTC	528
Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu	
165 170 175	
AAC AAC ACG CGG CCG CCG CGA GGC AAC TGG TTC GGC TGT ACA TGG ATG	576
Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met	
180 185 190	
AAT GGC ACT GGG TTC ACC AAG ACG TGT GGG GGC CCC CCG TGC AAC ATC	624
Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile	
195 200 205	
GGG GGG GCC GGC AAC AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT CGG	672
Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg	
210 215 220	
AAG CAC CCC GAG GCC ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG CTG	720

Met	Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Val	Val	Met	Leu	Leu	Phe	Ala
1				5					10					15	
Gly	Val	Asp	Gly	His	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Ala	Ser	Asp
			20					25					30		
Thr	Arg	Gly	Leu	Val	Ser	Leu	Phe	Ser	Pro	Gly	Ser	Ala	Gln	Lys	Ile
		35					40					45			
Gln	Leu	Val	Asn	Thr	Asn	Gly	Ser	Trp	His	Ile	Asn	Arg	Thr	Ala	Leu
	50					55					60				
Asn	Cys	Asn	Asp	Ser	Leu	Gln	Thr	Gly	Phe	Phe	Ala	Ala	Leu	Phe	Tyr
65					70					75					80
Lys	His	Lys	Phe	Asn	Ser	Ser	Gly	Cys	Pro	Glu	Arg	Leu	Ala	Ser	Cys
				85					90					95	
Arg	Ser	Ile	Asp	Lys	Phe	Ala	Gln	Gly	Trp	Gly	Pro	Leu	Thr	Tyr	Thr
		100						105					110		
Glu	Pro	Asn	Ser	Ser	Asp	Gln	Arg	Pro	Tyr	Cys	Trp	His	Tyr	Ala	Pro
		115					120					125			
Arg	Pro	Cys	Gly	Ile	Val	Pro	Ala	Ser	Gln	Val	Cys	Gly	Pro	Val	Tyr

130	135	140
Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly		
145	150	155 160
Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu		
	165	170 175
Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met		
	180	185 190
Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile		
	195	200 205
Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg		
	210	215 220
Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu		
	225	230 235 240
Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro		
	245	250 255
Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly		
	260	265 270
Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg		
	275	280 285
Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu		
	290	295 300
Ser Thr Thr Gly Asp Arg Gly Gln Thr Pro Ser Pro Pro Ser Leu		
305	310	315

(2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1395 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1392

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..1389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG GGC CTC GCC TAC TAT

Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	Ala	Gly	Leu	Ala	Tyr	Tyr	
1				5					10					15		
TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTT	TTG	GTT	GTG	ATG	CTA	CTC	TTT	96
Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Val	Val	Met	Leu	Leu	Phe	
			20					25					30			
GCC	GGC	GTC	GAC	GGG	CAT	ACC	CGC	GTG	TCA	GGA	GGG	GCA	GCA	GCC	TCC	144
Ala	Gly	Val	Asp	Gly	His	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Ala	Ser	
		35					40					45				
GAT	ACC	AGG	GGC	CTT	GTG	TCC	CTC	TTT	AGC	CCC	GGG	TCG	GCT	CAG	AAA	192
Asp	Thr	Arg	Gly	Leu	Val	Ser	Leu	Phe	Ser	Pro	Gly	Ser	Ala	Gln	Lys	
	50					55					60					
ATC	CAG	CTC	GTA	AAC	ACC	AAC	GGC	AGT	TGG	CAC	ATC	AAC	AGG	ACT	GCC	240
Ile	Gln	Leu	Val	Asn	Thr	Asn	Gly	Ser	Trp	His	Ile	Asn	Arg	Thr	Ala	
65					70				75						80	
CTG	AAC	TGC	AAC	GAC	TCC	CTC	CAA	ACA	GGG	TTC	TTT	GCC	GCA	CTA	TTC	288
Leu	Asn	Cys	Asn	Asp	Ser	Leu	Gln	Thr	Gly	Phe	Phe	Ala	Ala	Leu	Phe	
				85					90					95		
TAC	AAA	CAC	AAA	TTC	AAC	TCG	TCT	GGA	TGC	CCA	GAG	CGC	TTG	GCC	AGC	336
Tyr	Lys	His	Lys	Phe	Asn	Ser	Ser	Gly	Cys	Pro	Glu	Arg	Leu	Ala	Ser	
			100					105					110			
TGT	CGC	TCC	ATC	GAC	AAG	TTC	GCT	CAG	GGG	TGG	GGT	CCC	CTC	ACT	TAC	384
Cys	Arg	Ser	Ile	Asp	Lys	Phe	Ala	Gln	Gly	Trp	Gly	Pro	Leu	Thr	Tyr	
		115					120					125				
ACT	GAG	CCT	AAC	AGC	TCG	GAC	CAG	AGG	CCC	TAC	TGC	TGG	CAC	TAC	GCG	432
Thr	Glu	Pro	Asn	Ser	Ser	Asp	Gln	Arg	Pro	Tyr	Cys	Trp	His	Tyr	Ala	
	130					135					140					
CCT	CGA	CCG	TGT	GGT	ATT	GTA	CCC	GCG	TCT	CAG	GTG	TGC	GGT	CCA	GTG	480
Pro	Arg	Pro	Cys	Gly	Ile	Val	Pro	Ala	Ser	Gln	Val	Cys	Gly	Pro	Val	
145					150					155					160	
TAT	TGC	TTC	ACC	CCG	AGC	CCT	GTT	GTG	GTG	GGG	ACG	ACC	GAT	CGG	TTT	528
Tyr	Cys	Phe	Thr	Pro	Ser	Pro	Val	Val	Val	Gly	Thr	Thr	Asp	Arg	Phe	
				165					170					175		
GGT	GTC	CCC	ACG	TAT	AAC	TGG	GGG	GCG	AAC	GAC	TCG	GAT	GTG	CTG	ATT	576
Gly	Val	Pro	Thr	Tyr	Asn	Trp	Gly	Ala	Asn	Asp	Ser	Asp	Val	Leu	Ile	
			180					185					190			
CTC	AAC	AAC	ACG	CGG	CCG	CCG	CGA	GGC	AAC	TGG	TTC	GGC	TGT	ACA	TGG	624
Leu	Asn	Asn	Thr	Arg	Pro	Pro	Arg	Gly	Asn	Trp	Phe	Gly	Cys	Thr	Trp	
			195				200					205				
ATG	AAT	GGC	ACT	GGG	TTC	ACC	AAG	ACG	TGT	GGG	GGC	CCC	CCG	TGC	AAC	672
Met	Asn	Gly	Thr	Gly	Phe	Thr	Lys	Thr	Cys	Gly	Gly	Pro	Pro	Cys	Asn	
	210					215					220					
ATC	GGG	GGG	GCC	GGC	AAC	AAC	ACC	TTG	ACC	TGC	CCC	ACT	GAC	TGT	TTT	720
Ile	Gly	Gly	Ala	Gly	Asn	Asn	Thr	Leu	Thr	Cys	Pro	Thr	Asp	Cys	Phe	
225					230					235					240	
CGG	AAG	CAC	CCC	GAG	GCC	ACC	TAC	GCC	AGA	TGC	GGT	TCT	GGG	CCC	TGG	768
Arg	Lys	His	Pro	Glu	Ala	Thr	Tyr	Ala	Arg	Cys	Gly	Ser	Gly	Pro	Trp	
				245					250					255		

CTG ACA CCT AGG TGT ATG GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC	816
Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr	
260 265 270	
CCC TGC ACT GTC AAC TTC ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG	864
Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly	
275 280 285	
GGC GTG GAG CAC AGG TTC GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG	912
Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu	
290 295 300	
CGT TGT GAC TTG GAG GAC AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG	960
Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu	
305 310 315 320	
CTG TCT ACA ACA GAG TGG CAG ATA CTG CCC TGT TCC TTC ACC ACC CTG	1008
Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu	
325 330 335	
CCG GCC CTA TCC ACC GGC CTG ATC CAC CTC CAT CAG AAC ATC GTG GAC	1056
Pro Ala Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp	
340 345 350	
GTG CAA TAC CTG TAC GGT GTA GGG TCG GCG GTT GTC TCC CTT GTC ATC	1104
Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val Val Ser Leu Val Ile	
355 360 365	
AAA TGG GAG TAT GTC CTG TTG CTC TTC CTT CTC CTG GCA GAC GCG CGC	1152
Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu Ala Asp Ala Arg	
370 375 380	
ATC TGC GCC TGC TTA TGG ATG ATG CTG CTG ATA GCT CAA GCT GAG GCC	1200
Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala	
385 390 395 400	
GCC TTA GAG AAC CTG GTG GTC CTC AAT GCG GCG GCC GTG GCC GGG GCG	1248
Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala Ala Val Ala Gly Ala	
405 410 415	
CAT GGC ACT CTT TCC TTC CTT GTG TTC TTC TGT GCT GCC TGG TAC ATC	1296
His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile	
420 425 430	
AAG GGC AGG CTG GTC CCT GGT GCG GCA TAC GCC TTC TAT GGC GTG TGG	1344
Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp	
435 440 445	
CCG CTG CTC CTG CTT CTG CTG GCC TTA CCA CCA CGA GCT TAT GCC TAGTAA	1395
Pro Leu Leu Leu Leu Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala	
450 455 460	

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	Ala	Gly	Leu	Ala	Tyr	Tyr	1	5	10	15
Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Val	Val	Met	Leu	Leu	Phe	20	25	30	
Ala	Gly	Val	Asp	Gly	His	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Ala	Ser	35	40	45	
Asp	Thr	Arg	Gly	Leu	Val	Ser	Leu	Phe	Ser	Pro	Gly	Ser	Ala	Gln	Lys	50	55	60	
Ile	Gln	Leu	Val	Asn	Thr	Asn	Gly	Ser	Trp	His	Ile	Asn	Arg	Thr	Ala	65	70	75	80
Leu	Asn	Cys	Asn	Asp	Ser	Leu	Gln	Thr	Gly	Phe	Phe	Ala	Ala	Leu	Phe	85	90	95	
Tyr	Lys	His	Lys	Phe	Asn	Ser	Ser	Gly	Cys	Pro	Glu	Arg	Leu	Ala	Ser	100	105	110	
Cys	Arg	Ser	Ile	Asp	Lys	Phe	Ala	Gln	Gly	Trp	Gly	Pro	Leu	Thr	Tyr	115	120	125	
Thr	Glu	Pro	Asn	Ser	Ser	Asp	Gln	Arg	Pro	Tyr	Cys	Trp	His	Tyr	Ala	130	135	140	
Pro	Arg	Pro	Cys	Gly	Ile	Val	Pro	Ala	Ser	Gln	Val	Cys	Gly	Pro	Val	145	150	155	160
Tyr	Cys	Phe	Thr	Pro	Ser	Pro	Val	Val	Val	Gly	Thr	Thr	Asp	Arg	Phe	165	170	175	
Gly	Val	Pro	Thr	Tyr	Asn	Trp	Gly	Ala	Asn	Asp	Ser	Asp	Val	Leu	Ile	180	185	190	
Leu	Asn	Asn	Thr	Arg	Pro	Pro	Arg	Gly	Asn	Trp	Phe	Gly	Cys	Thr	Trp	195	200	205	
Met	Asn	Gly	Thr	Gly	Phe	Thr	Lys	Thr	Cys	Gly	Gly	Pro	Pro	Cys	Asn	210	215	220	
Ile	Gly	Gly	Ala	Gly	Asn	Asn	Thr	Leu	Thr	Cys	Pro	Thr	Asp	Cys	Phe	225	230	235	240
Arg	Lys	His	Pro	Glu	Ala	Thr	Tyr	Ala	Arg	Cys	Gly	Ser	Gly	Pro	Trp	245	250	255	
Leu	Thr	Pro	Arg	Cys	Met	Val	His	Tyr	Pro	Tyr	Arg	Leu	Trp	His	Tyr	260	265	270	
Pro	Cys	Thr	Val	Asn	Phe	Thr	Ile	Phe	Lys	Val	Arg	Met	Tyr	Val	Gly	275	280	285	
Gly	Val	Glu	His	Arg	Phe	Glu	Ala	Ala	Cys	Asn	Trp	Thr	Arg	Gly	Glu	290	295	300	
Arg	Cys	Asp	Leu	Glu	Asp	Arg	Asp	Arg	Ser	Glu	Leu	Ser	Pro	Leu	Leu	305	310	315	320

Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu
 325 330 335
 Pro Ala Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp
 340 345 350
 Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val Val Ser Leu Val Ile
 355 360 365
 Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg
 370 375 380
 Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala
 385 390 395 400
 Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala Ala Val Ala Gly Ala
 405 410 415
 His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile
 420 425 430
 Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp
 435 440 445
 Pro Leu Leu Leu Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala
 450 455 460

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2079

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..2076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

AAT TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Thr Leu Gly Gly Ala Ala Arg	
20 25 30	

GCC	CTG	GCG	CAT	GGC	GTC	CGG	GTT	CTG	GAG	GAC	GGC	GTG	AAC	TAT	GCA	144
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	
		35					40					45				
ACA	GGG	AAT	TTG	CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	TTG	GCT	TTG	192
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	
		50				55					60					
CTG	TCC	TGT	CTG	ACC	GTT	CCA	GCT	TCC	GCT	TAT	GAA	GTG	CGC	AAC	GTG	240
Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	
		65			70					75					80	
TCC	GGG	ATG	TAC	CAT	GTC	ACG	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATT	GTG	288
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	
				85					90					95		
TAT	GAG	GCA	GCG	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	336
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	
			100					105					110			
GTT	CGG	GAG	AAC	AAC	TCT	TCC	CGC	TGC	TGG	GTA	GCG	CTC	ACC	CCC	ACG	384
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	
		115					120					125				
CTC	GCA	GCT	AGG	AAC	GCC	AGC	GTC	CCC	ACC	ACG	ACA	ATA	CGA	CGC	CAC	432
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	
		130				135					140					
GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	GCT	TTC	TGT	TCC	GCT	ATG	TAC	GTG	480
Val	Asp	Leu	Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	
	145				150				155						160	
GGG	GAC	CTC	TGC	GGA	TCT	GTC	TTC	CTC	GTC	TCC	CAG	CTG	TTC	ACC	ATC	528
Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile	
			165						170					175		
TCG	CCT	CGC	CGG	CAT	GAG	ACG	GTG	CAG	GAC	TGC	AAT	TGC	TCA	ATC	TAT	576
Ser	Pro	Arg	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	
			180					185					190			
CCC	GGC	CAC	ATA	ACG	GGT	CAC	CGT	ATG	GCT	TGG	GAT	ATG	ATG	ATG	AAC	624
Pro	Gly	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	
		195					200					205				
TGG	TCG	CCT	ACA	ACG	GCC	CTG	GTG	GTA	TCG	CAG	CTG	CTC	CGG	ATC	CCA	672
Trp	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro	
		210				215						220				
CAA	GCT	GTC	GTG	GAC	ATG	GTG	GCG	GGG	GCC	CAT	TGG	GGA	GTC	CTG	GCG	720
Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	Ala	
	225				230					235					240	
GGC	CTC	GCC	TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTT	TTG	GTT	768
Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Val	
			245						250					255		
GTG	ATG	CTA	CTC	TTT	GCC	GGC	GTC	GAC	GGG	CAT	ACC	CGC	GTG	TCA	GGA	816
Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly	His	Thr	Arg	Val	Ser	Gly	
			260					265					270			
GGG	GCA	GCA	GCC	TCC	GAT	ACC	AGG	GGC	CTT	GTG	TCC	CTC	TTT	AGC	CCC	864
Gly	Ala	Ala	Ala	Ser	Asp	Thr	Arg	Gly	Leu	Val	Ser	Leu	Phe	Ser	Pro	

275	280	285	
GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC ACC AAC GGC AGT TGG CAC Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His 290 295 300			912
ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC TCC CTC CAA ACA GGG TTC Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe 305 310 315 320			960
TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC AAC TCG TCT GGA TGC CCA Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly Cys Pro 325 330 335			1008
GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC AAG TTC GCT CAG GGG TGG Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp 340 345 350			1056
GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC TCG GAC CAG AGG CCC TAC Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr 355 360 365			1104
TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT ATT GTA CCC GCG TCT CAG Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln 370 375 380			1152
GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG AGC CCT GTT GTG GTG GGG Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly 385 390 395 400			1200
ACG ACC GAT CGG TTT GGT GTC CCC ACG TAT AAC TGG GGG GCG AAC GAC Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp 405 410 415			1248
TCG GAT GTG CTG ATT CTC AAC AAC ACG CCG CCG CCG CGA GGC AAC TGG Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp 420 425 430			1296
TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC ACC AAG ACG TGT GGG Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly 435 440 445			1344
GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC AAC ACC TTG ACC TGC Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys 450 455 460			1392
CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG GCC ACC TAC GCC AGA TGC Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala Arg Cys 465 470 475 480			1440
GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT ATG GTT CAT TAC CCA TAT Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr 485 490 495			1488
AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC TTC ACC ATC TTC AAG GTT Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val 500 505 510			1536
AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG TTC GAA GCC GCA TGC AAT Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn 515 520 525			1584
TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC AGG GAT AGA TCA GAG			1632

Trp	Thr	Arg	Gly	Glu	Arg	Cys	Asp	Leu	Glu	Asp	Arg	Asp	Arg	Ser	Glu		
530						535					540						
CTT	AGC	CCG	CTG	CTG	CTG	TCT	ACA	ACA	GAG	TGG	CAG	ATA	CTG	CCC	TGT	1680	
Leu	Ser	Pro	Leu	Leu	Leu	Ser	Thr	Thr	Glu	Trp	Gln	Ile	Leu	Pro	Cys		
545					550					555					560		
TCC	TTC	ACC	ACC	CTG	CCG	GCC	CTA	TCC	ACC	GGC	CTG	ATC	CAC	CTC	CAT	1728	
Ser	Phe	Thr	Thr	Leu	Pro	Ala	Leu	Ser	Thr	Gly	Leu	Ile	His	Leu	His		
				565					570					575			
CAG	AAC	ATC	GTG	GAC	GTG	CAA	TAC	CTG	TAC	GGT	GTA	GGG	TCG	GCG	GTT	1776	
Gln	Asn	Ile	Val	Asp	Val	Gln	Tyr	Leu	Tyr	Gly	Val	Gly	Ser	Ala	Val		
			580					585					590				
GTC	TCC	CTT	GTC	ATC	AAA	TGG	GAG	TAT	GTC	CTG	TTG	CTC	TTC	CTT	CTC	1824	
Val	Ser	Leu	Val	Ile	Lys	Trp	Glu	Tyr	Val	Leu	Leu	Leu	Phe	Leu	Leu		
		595					600					605					
CTG	GCA	GAC	GCG	CGC	ATC	TGC	GCC	TGC	TTA	TGG	ATG	ATG	CTG	CTG	ATA	1872	
Leu	Ala	Asp	Ala	Arg	Ile	Cys	Ala	Cys	Leu	Trp	Met	Met	Leu	Leu	Ile		
	610					615					620						
GCT	CAA	GCT	GAG	GCC	GCC	TTA	GAG	AAC	CTG	GTG	GTC	CTC	AAT	GCG	GCG	1920	
Ala	Gln	Ala	Glu	Ala	Ala	Leu	Glu	Asn	Leu	Val	Val	Leu	Asn	Ala	Ala		
	625				630					635					640		
GCC	GTG	GCC	GGG	GCG	CAT	GGC	ACT	CTT	TCC	TTC	CTT	GTG	TTC	TTC	TGT	1968	
Ala	Val	Ala	Gly	Ala	His	Gly	Thr	Leu	Ser	Phe	Leu	Val	Phe	Phe	Cys		
				645					650					655			
GCT	GCC	TGG	TAC	ATC	AAG	GGC	AGG	CTG	GTC	CCT	GGT	GCG	GCA	TAC	GCC	2016	
Ala	Ala	Trp	Tyr	Ile	Lys	Gly	Arg	Leu	Val	Pro	Gly	Ala	Ala	Tyr	Ala		
			660					665					670				
TTC	TAT	GGC	GTG	TGG	CCG	CTG	CTC	CTG	CTT	CTG	CTG	GCC	TTA	CCA	CCA	2064	
Phe	Tyr	Gly	Val	Trp	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Leu	Pro	Pro		
		675				680						685					
CGA	GCT	TAT	GCC	TAGTAA												2082	
Arg	Ala	Tyr	Ala														
			690														

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 692 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu		
1				5				10						15			
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg		
		20					25						30				
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala		

35					40					45					
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu
50						55					60				
Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val
65					70					75					80
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val
				85					90					95	
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys
			100					105					110		
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr
		115					120					125			
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His
		130					135					140			
Val	Asp	Leu	Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val
145					150					155					160
Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile
			165						170					175	
Ser	Pro	Arg	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr
			180					185					190		
Pro	Gly	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn
		195					200					205			
Trp	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro
		210				215					220				
Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	Ala
225					230					235					240
Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Val
			245						250					255	
Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly	His	Thr	Arg	Val	Ser	Gly
		260						265					270		
Gly	Ala	Ala	Ala	Ser	Asp	Thr	Arg	Gly	Leu	Val	Ser	Leu	Phe	Ser	Pro
		275					280						285		
Gly	Ser	Ala	Gln	Lys	Ile	Gln	Leu	Val	Asn	Thr	Asn	Gly	Ser	Trp	His
	290					295					300				
Ile	Asn	Arg	Thr	Ala	Leu	Asn	Cys	Asn	Asp	Ser	Leu	Gln	Thr	Gly	Phe
305					310					315					320
Phe	Ala	Ala	Leu	Phe	Tyr	Lys	His	Lys	Phe	Asn	Ser	Ser	Gly	Cys	Pro
			325						330					335	
Glu	Arg	Leu	Ala	Ser	Cys	Arg	Ser	Ile	Asp	Lys	Phe	Ala	Gln	Gly	Trp
		340						345					350		
Gly	Pro	Leu	Thr	Tyr	Thr	Glu	Pro	Asn	Ser	Ser	Asp	Gln	Arg	Pro	Tyr
	355						360					365			
Cys	Trp	His	Tyr	Ala	Pro	Arg	Pro	Cys	Gly	Ile	Val	Pro	Ala	Ser	Gln

370	375	380
Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly 385 390 395 400		
Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp 405 410 415		
Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp 420 425 430		
Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly 435 440 445		
Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys 450 455 460		
Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala Arg Cys 465 470 475 480		
Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr 485 490 495		
Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val 500 505 510		
Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn 515 520 525		
Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu 530 535 540		
Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys 545 550 555 560		
Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly Leu Ile His Leu His 565 570 575		
Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val 580 585 590		
Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu 595 600 605		
Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile 610 615 620		
Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala 625 630 635 640		
Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys 645 650 655		
Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala 660 665 670		
Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu Leu Leu Ala Leu Pro Pro 675 680 685		
Arg Ala Tyr Ala 690		

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2430

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..2427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC	48
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT GGT	96
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly	
20 25 30	
GGA GTT TAC CTG TTG CCG CGC AGG GGC CCC AGG TTG GGT GTG CGC GCG	144
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	
35 40 45	
ACT AGG AAG ACT TCC GAG CGG TCG CAA CCT CGT GGG AGG CGA CAA CCT	192
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	
50 55 60	
ATC CCC AAG GCT CGC CGA CCC GAG GGT AGG GCC TGG GCT CAG CCC GGG	240
Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly	
65 70 75 80	
TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC ATG GGG TGG GCA GGA TGG	288
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp	
85 90 95	
CTC CTG TCA CCC CGC GGC TCT CGG CCT AGT TGG GGC CCT ACA GAC CCC	336
Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro	
100 105 110	
CGG CGT AGG TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC	384
Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys	
115 120 125	
GGC TTC GCC GAC CTC GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA	432
Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu	
130 135 140	
GGG GGC GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC	480

Gly	Gly	Ala	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	
145					150				155					160		
GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAT	TTG	CCC	GGT	TGC	TCT	TTC	TCT	ATC	528
Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	
				165				170						175		
TTC	CTC	TTG	GCT	TTG	CTG	TCC	TGT	CTG	ACC	GTT	CCA	GCT	TCC	GCT	TAT	576
Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	
			180					185					190			
GAA	GTG	CGC	AAC	GTG	TCC	GGG	ATG	TAC	CAT	GTC	ACG	AAC	GAC	TGC	TCC	624
Glu	Val	Arg	Asn	Val	Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	
		195				200						205				
AAC	TCA	AGC	ATT	GTG	TAT	GAG	GCA	GCG	GAC	ATG	ATC	ATG	CAC	ACC	CCC	672
Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	
	210					215					220					
GGG	TGC	GTG	CCC	TGC	GTT	CGG	GAG	AAC	AAC	TCT	TCC	CGC	TGC	TGG	GTA	720
Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	
225					230					235				240		
GCG	CTC	ACC	CCC	ACG	CTC	GCA	GCT	AGG	AAC	GCC	AGC	GTC	CCC	ACC	ACG	768
Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	
				245					250					255		
ACA	ATA	CGA	CGC	CAC	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	GCT	TTC	TGT	816
Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	
			260					265					270			
TCC	GCT	ATG	TAC	GTG	GGG	GAC	CTC	TGC	GGA	TCT	GTC	TTC	CTC	GTC	TCC	864
Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	
		275					280					285				
CAG	CTG	TTC	ACC	ATC	TCG	CCT	CGC	CGG	CAT	GAG	ACG	GTG	CAG	GAC	TGC	912
Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	
	290					295					300					
AAT	TGC	TCA	ATC	TAT	CCC	GGC	CAC	ATA	ACG	GGT	CAC	CGT	ATG	GCT	TGG	960
Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	
305					310					315				320		
GAT	ATG	ATG	ATG	AAC	TGG	TCG	CCT	ACA	ACG	GCC	CTG	GTG	GTA	TCG	CAG	1008
Asp	Met	Met	Met	Asn	Trp	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	
				325					330					335		
CTG	CTC	CGG	ATC	CCA	CAA	GCT	GTC	GTG	GAC	ATG	GTG	GCG	GGG	GCC	CAT	1056
Leu	Leu	Arg	Ile	Pro	Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His	
			340					345					350			
TGG	GGA	GTC	CTG	GCG	GGC	CTC	GCC	TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	1104
Trp	Gly	Val	Leu	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	
	355						360					365				
GCT	AAG	GTT	TTG	GTT	GTG	ATG	CTA	CTC	TTT	GCC	GGC	GTC	GAC	GGG	CAT	1152
Ala	Lys	Val	Leu	Val	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly	His	
	370					375					380					
ACC	CGC	GTG	TCA	GGA	GGG	GCA	GCA	GCC	TCC	GAT	ACC	AGG	GGC	CTT	GTG	1200
Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Ala	Ser	Asp	Thr	Arg	Gly	Leu	Val	
385					390					395				400		

TCC CTC TTT AGC CCC GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC ACC	1248
Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr	
405 410 415	
AAC GGC AGT TGG CAC ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC TCC	1296
Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser	
420 425 430	
CTC CAA ACA GGG TTC TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC AAC	1344
Leu Gln Thr Gly Phe Phe Ala Leu Phe Tyr Lys His Lys Phe Asn	
435 440 445	
TCG TCT GGA TGC CCA GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC AAG	1392
Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys	
450 455 460	
TTC GCT CAG GGG TGG GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC TCG	1440
Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser	
465 470 475 480	
GAC CAG AGG CCC TAC TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT ATT	1488
Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile	
485 490 495	
GTA CCC GCG TCT CAG GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG AGC	1536
Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser	
500 505 510	
CCT GTT GTG GTG GGG ACG ACC GAT CCG TTT GGT GTC CCC ACG TAT AAC	1584
Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn	
515 520 525	
TGG GGG GCG AAC GAC TCG GAT GTG CTG ATT CTC AAC AAC ACG CCG CCG	1632
Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro	
530 535 540	
CCG CGA GGC AAC TGG TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC	1680
Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe	
545 550 555 560	
ACC AAG ACG TGT GGG GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC	1728
Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn	
565 570 575	
AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG GCC	1776
Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala	
580 585 590	
ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT ATG	1824
Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met	
595 600 605	
GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC TTC	1872
Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe	
610 615 620	
ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG TTC	1920
Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe	
625 630 635 640	
GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC	1968

Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp	
645	650 655
AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG TCT ACA ACA GAG TGG	2016
Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp	
660	665 670
CAG ATA CTG CCC TGT TCC TTC ACC ACC CTG CCG GCC CTA TCC ACC GGC	2064
Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly	
675	680 685
CTG ATC CAC CTC CAT CAG AAC ATC GTG GAC GTG CAA TAC CTG TAC GGT	2112
Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly	
690	695 700
GTA GGG TCG GCG GTT GTC TCC CTT GTC ATC AAA TGG GAG TAT GTC CTG	2160
Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu	
705	710 715 720
TTG CTC TTC CTT CTC CTG GCA GAC GCG CGC ATC TGC GCC TGC TTA TGG	2208
Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp	
725	730 735
ATG ATG CTG CTG ATA GCT CAA GCT GAG GCC GCC TTA GAG AAC CTG GTG	2256
Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val	
740	745 750
GTC CTC AAT GCG GCG GCC GTG GCC GGG GCG CAT GGC ACT CTT TCC TTC	2304
Val Leu Asn Ala Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe	
755	760 765
CTT GTG TTC TTC TGT GCT GCC TGG TAC ATC AAG GGC AGG CTG GTC CCT	2352
Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro	
770	775 780
GGT GCG GCA TAC GCC TTC TAT GGC GTG TGG CCG CTG CTC CTG CTT CTG	2400
Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu Leu	
785	790 795 800
CTG GCC TTA CCA CCA CGA GCT TAT GCC TAGTAA	2433
Leu Ala Leu Pro Pro Arg Ala Tyr Ala	
805	810

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn
1				5					10					15	
Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly
		20						25					30		
Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala

35					40					45					
Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro
50						55					60				
Ile	Pro	Lys	Ala	Arg	Arg	Pro	Glu	Gly	Arg	Ala	Trp	Ala	Gln	Pro	Gly
65					70					75					80
Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Met	Gly	Trp	Ala	Gly	Trp
				85					90					95	
Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Thr	Asp	Pro
			100					105					110		
Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys
		115				120					125				
Gly	Phe	Ala	Asp	Leu	Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu
	130					135					140				
Gly	Gly	Ala	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp
145					150					155					160
Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile
				165					170					175	
Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr
			180					185					190		
Glu	Val	Arg	Asn	Val	Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser
		195					200					205			
Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro
		210				215					220				
Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val
225					230					235					240
Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr
				245					250					255	
Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys
			260					265					270		
Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser
		275					280					285			
Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	Arg	His	Glu	Thr	Val	Gln	Asp	Cys
	290					295					300				
Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp
305					310					315					320
Asp	Met	Met	Met	Asn	Trp	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln
				325					330					335	
Leu	Leu	Arg	Ile	Pro	Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His
			340					345					350		
Trp	Gly	Val	Leu	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp
	355						360					365			
Ala	Lys	Val	Leu	Val	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly	His

370	375	380
Thr Arg Val Ser Gly 385	Gly Ala Ala Ala Ser 390	Asp Thr Arg Gly Leu Val 395 400
Ser Leu Phe Ser Pro 405	Gly Ser Ala Gln Lys 410	Ile Gln Leu Val Asn Thr 415
Asn Gly Ser Trp His 420	Ile Asn Arg Thr Ala 425	Leu Asn Cys Asn Asp Ser 430
Leu Gln Thr Gly Phe 435	Phe Ala Ala Leu Phe 440	Tyr Lys His Lys Phe Asn 445
Ser Ser Gly Cys Pro 450	Glu Arg Leu Ala Ser 455	Cys Arg Ser Ile Asp Lys 460
Phe Ala Gln Gly Trp 465	Gly Pro Leu Thr Tyr 470	Thr Glu Pro Asn Ser Ser 475 480
Asp Gln Arg Pro Tyr 485	Cys Trp His Tyr Ala 490	Pro Arg Pro Cys Gly Ile 495
Val Pro Ala Ser Gln 500	Val Cys Gly Pro Val 505	Tyr Cys Phe Thr Pro Ser 510
Pro Val Val Val Gly 515	Thr Thr Asp Arg Phe 520	Gly Val Pro Thr Tyr Asn 525
Trp Gly Ala Asn Asp 530	Ser Asp Val Leu Ile 535	Leu Asn Thr Arg Pro 540
Pro Arg Gly Asn Trp 545	Phe Gly Cys Thr Trp 550	Met Asn Gly Thr Gly Phe 555 560
Thr Lys Thr Cys Gly 565	Gly Pro Pro Cys Asn 570	Ile Gly Gly Ala Gly Asn 575
Asn Thr Leu Thr Cys 580	Pro Thr Asp Cys Phe 585	Arg Lys His Pro Glu Ala 590
Thr Tyr Ala Arg Cys 595	Gly Ser Gly Pro Trp 600	Leu Thr Pro Arg Cys Met 605
Val His Tyr Pro Tyr 610	Arg Leu Trp His Tyr 615	Pro Cys Thr Val Asn Phe 620
Thr Ile Phe Lys Val 625	Arg Met Tyr Val Gly 630	Gly Val Glu His Arg Phe 635 640
Glu Ala Ala Cys Asn 645	Trp Thr Arg Gly Glu 650	Arg Cys Asp Leu Glu Asp 655
Arg Asp Arg Ser Glu 660	Leu Ser Pro Leu Leu 665	Ser Thr Thr Glu Trp 670
Gln Ile Leu Pro Cys 675	Ser Phe Thr Thr Leu 680	Pro Ala Leu Ser Thr Gly 685
Leu Ile His Leu His 690	Gln Asn Ile Val Asp 695	Val Gln Tyr Leu Tyr Gly 700

Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu
 705 710 715 720

Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp
 725 730 735

Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val
 740 745 750

Val Leu Asn Ala Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe
 755 760 765

Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro
 770 775 780

Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu Leu
 785 790 795 800

Leu Ala Leu Pro Pro Arg Ala Tyr Ala
 805

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1..17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Ser Asn Ser Ser Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys
 1 5 10 15

Val

(2) INFORMATION FOR SEQ ID NO: 52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1..22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Gly Gly Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 1 5 10 15

Ser Pro Thr Thr Ala Leu
 20

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..37

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys
 1 5 10 15

Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr
 20 25 30

Pro Gly Cys Gly Lys
 35

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Gly Gly Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Ala Thr
 1 5 10 15

Gln Leu Arg Arg His Ile Asp Leu Leu
 20 25

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```

Gly Gly Thr Pro Thr Leu Ala Ala Arg Asp Ala Ser Val Pro Thr Thr
1           5           10           15
Thr Ile Arg Arg His Val Asp Leu Leu
          20           25

```

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

```

Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Gln Val Arg Asn
1           5           10           15
Ser Thr Gly Leu
          20

```

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```

Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp Cys Pro
1           5           10           15
Asn Ser Ser Ile
          20

```


(2) INFORMATION FOR SEQ ID NO: 58:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala His Asp Ala Ile
 1 5 10 15
 Leu His Thr Pro
 20

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr
 1 5 10 15
 Pro Gly Cys Val
 20

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

His Asp Ala Ile Leu His Thr Pro Gly Val Pro Cys Val Arg Glu Gly
 1 5 10 15
 Asn Val Ser

(2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

Cys Val Arg Glu Gly Asn Val Ser Arg Cys Trp Val Ala Met Thr Pro
 1 5 10 15

Thr Val Ala Thr
 20

(2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

Ala Met Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Ala Thr
 1 5 10 15

Gln Leu Arg Arg
 20

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser
 1 5 10 15

Ala Thr Leu Cys
 20

(2) INFORMATION FOR SEQ ID NO: 64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

Leu	Val	Gly	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu
1				5				10					15		
Cys Gly Ser Val															
20															

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg	Arg	His	Trp	Thr	Thr	Gln	Gly	Cys
1				5					10				15		
Asn Cys Ser Ile															
20															

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

Thr	Gln	Gly	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	Ile	Thr	Gly	His
1				5					10					15	
Arg Met Ala Trp															
20															

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

```

Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro
1           5           10           15

Thr Ala Ala Leu
                20

```

(2) INFORMATION FOR SEQ ID NO: 68:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

```

Asn Trp Ser Pro Thr Ala Ala Leu Val Met Ala Gln Leu Leu Arg Ile
1           5           10           15

Pro Gln Ala Ile
                20

```

(2) INFORMATION FOR SEQ ID NO: 69:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

```

Leu Leu Arg Ile Pro Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His
1           5           10           15

Trp Gly Val Leu
                20

```

(2) INFORMATION FOR SEQ ID NO: 70:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

Ala Gly Ala His Trp Gly Val Leu Ala Gly Ile Ala Tyr Phe Ser Met
 1 5 10 15
 Val Gly Asn Met
 20

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala Glu Thr Ile Val Ser
 1 5 10 15
 Gly Gly Gln Ala
 20

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

Ser Gly Leu Val Ser Leu Phe Thr Pro Gly Ala Lys Gln Asn Ile Gln
 1 5 10 15
 Leu Ile Asn Thr
 20

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

Gln Asn Ile Gln Leu Ile Asn Thr Asn Gly Gln Trp His Ile Asn Ser
1 5 10 15

Thr Ala Leu Asn
20

(2) INFORMATION FOR SEQ ID NO: 74:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

Leu Asn Cys Asn Glu Ser Leu Asn Thr Gly Trp Trp Leu Ala Gly Leu
1 5 10 15

Ile Tyr Gln His Lys
20

(2) INFORMATION FOR SEQ ID NO: 75:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

Ala Gly Leu Ile Tyr Gln His Lys Phe Asn Ser Ser Gly Cys Pro Glu
1 5 10 15

Arg Leu Ala Ser
20

(2) INFORMATION FOR SEQ ID NO: 76:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Pro Leu Thr Asp Phe Asp

1 5 10 15
 Gln Gly Trp Gly
 20

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

Thr Asp Phe Asp Gln Gly Trp Gly Pro Ile Ser Tyr Ala Asn Gly Ser
 1 5 10 15

Gly Pro Asp Gln
 20

(2) INFORMATION FOR SEQ ID NO: 78:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

Ala Asn Gly Ser Gly Pro Asp Gln Arg Pro Tyr Cys Trp His Tyr Pro
 1 5 10 15

Pro Lys Pro Cys
 20

(2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

Trp His Tyr Pro Pro Lys Pro Cys Gly Ile Val Pro Ala Lys Ser Val
 1 5 10 15

Cys Gly Pro Val

20

(2) INFORMATION FOR SEQ ID NO: 80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

Ala Lys Ser Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val
 1 5 10 15
 Val Val Gly Thr
 20

(2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Ser Gly Ala Pro Thr
 1 5 10 15
 Tyr Ser Trp Gly
 20

(2) INFORMATION FOR SEQ ID NO: 82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

Gly Ala Pro Thr Tyr Ser Trp Gly Glu Asn Asp Thr Asp Val Phe Val
 1 5 10 15
 Leu Asn Asn Thr
 20

(2) INFORMATION FOR SEQ ID NO: 83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

Gly	Asn	Trp	Phe	Gly	Cys	Thr	Trp	Met	Asn	Ser	Thr	Gly	Phe	Thr	Lys
1				5					10					15	
Val Cys Gly Ala															
20															

(2) INFORMATION FOR SEQ ID NO: 84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Gly	Phe	Thr	Lys	Val	Cys	Gly	Ala	Pro	Pro	Val	Cys	Ile	Gly	Gly	Ala
1				5					10					15	
Gly Asn Asn Thr															
20															

(2) INFORMATION FOR SEQ ID NO: 85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

Ile	Gly	Gly	Ala	Gly	Asn	Asn	Thr	Leu	His	Cys	Pro	Thr	Asp	Cys	Arg
1				5					10					15	
Lys His Pro															

(2) INFORMATION FOR SEQ ID NO: 86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Thr	Asp	Cys	Phe	Arg	Lys	His	Pro	Asp	Ala	Thr	Tyr	Ser	Arg	Cys	Gly
1				5					10					15	

Ser	Gly	Pro	Trp
			20

(2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

Ser	Arg	Cys	Gly	Ser	Gly	Pro	Trp	Ile	Thr	Pro	Arg	Cys	Leu	Val	Asp
1				5					10					15	

Tyr	Pro	Tyr	Arg
			20

(2) INFORMATION FOR SEQ ID NO: 88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Cys	Leu	Val	Asp	Tyr	Pro	Tyr	Arg	Leu	Trp	His	Tyr	Pro	Cys	Thr	Ile
1				5					10					15	

Asn	Tyr	Thr	Ile
			20

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

Pro Cys Thr Ile Asn Tyr Thr Ile Phe Lys Ile Arg Met Tyr Val Gly
 1 5 10 15
 Gly Val Glu His
 20

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Met Tyr Val Gly Gly Val Glu His Arg Leu Glu Ala Ala Cys Asn Trp
 1 5 10 15
 Thr Pro Gly Glu
 20

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

Ala Cys Asn Trp Thr Pro Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp
 1 5 10 15
 Arg Ser Glu Leu
 20

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Thr Thr Thr
 1 5 10 15
 Gln Trp Gln Val
 20

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

Tyr Gln Val Arg Asn Ser Thr Gly Leu
 1 5

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

ACGTCCGTAC GTTCGAATTA ATTAATCGA

29

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

CCTCCGGACG TGCCTAGCT CCCGTCTGTG GTAGTGGTGG TAGTGATTAT CAATTAATTG 60

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

GTTTAACCAC TGCATGATG 19

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

GTCCCATCGA GTGCGGCTAC 20

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

CGTGACATGG TACATTCCGG ACACTTGGCG CACTTCATAA GCGGA

45

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

TGCCTCATAC ACAATGGAGC TCTGGGACGA GTCGTTCTG AC

42

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

TACCCAGCAG CGGGAGCTCT GTTGCTCCCG AACGCAGGGC AC

42

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

TGTCGTGGTG GGGACGGAGG CCTGCCTAGC TGCGAGCGTG GG

42

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

CGTTATGTGG CCCGGGTAGA TTGAGCACTG GCAGTCCTGC ACCGTCTC

48

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

CAGGGCCGTT CTAGGCCTCC ACTGCATCAT CATATCCCAA GC

42

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

CCGGAATGTA CCATGTCACG AACGAC

26

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:
GCTCCATTGT GTATGAGGCA GCGG

24

(2) INFORMATION FOR SEQ ID NO: 106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:
GAGCTCCCGC TGCTGGGTAG CGC

23

(2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:
CCTCCGTCCC CACCACGACA ATACG

25

(2) INFORMATION FOR SEQ ID NO: 108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

CTACCCGGGC CACATAACGG GTCACCG

27

(2) INFORMATION FOR SEQ ID NO: 109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

GGAGGCCTAC AACGGCCCTG GTGG

24

(2) INFORMATION FOR SEQ ID NO: 110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

TTCTATCGAT TAAATAGAAT TC

22

(2) INFORMATION FOR SEQ ID NO: 111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

GCCATACGCT CACAGCCGAT CCC

(2) INFORMATION FOR SEQ ID NO: 112:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys
 1 5 10 15
 Ser Asn Ser Ser
 20

(2) INFORMATION FOR SEQ ID NO: 113:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp
 1 5 10 15
 Met Ile Met His Thr
 20

(2) INFORMATION FOR SEQ ID NO: 114:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val
 1 5 10 15

Arg Glu Asn Asn Ser
20

(2) INFORMATION FOR SEQ ID NO: 115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

Pro Cys Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu
1 5 10 15

Thr Pro Thr Leu Ala
20

(2) INFORMATION FOR SEQ ID NO: 116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala Ser Val Pro
1 5 10 15

Thr Thr Thr Ile Arg
20

(2) INFORMATION FOR SEQ ID NO: 117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
1 5 10 15

Gly Ala Ala Ala Phe
20

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly
1 5 10 15

Asp Leu Cys Gly Ser
20

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

Tyr Val Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu
1 5 10 15

Phe Thr Ile Ser Pro
20

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	Arg	His	Glu	Thr	Val	Gln
1					5				10					15
Asp Cys Asn Cys Ser														
20														

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	Ile	Thr
1					5				10					15
Gly His Arg Met Ala														
20														

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
1					5				10					15
Ser Pro Thr Thr Ala														
20														